JOURNAL OF CLINICAL MICROBIOLOGY, Nov. 1995, p. 3044–3046 Vol. 33, No. 11
0095-1137/95/$04.00+0

Comparison of MicroScan WalkAway System and Vitek System for Identification of Gram-Negative Bacteria

SANDRA RHOADS,[1] LESLIE MARINELLI,[1] CAROL ANN IMPERATRICE,[1] AND IRVING NACHAMKIN[1,2]*

Clinical Microbiology Laboratory,[1] Department of Pathology and Laboratory Medicine, University of Pennsylvania Medical Center and School of Medicine,[2] Philadelphia, Pennsylvania 19104-4283

Received 14 June 1995/Returned for modification 13 July 1995/Accepted 9 August 1995

In a prospective side-by-side comparison conducted from September through November 1994, we compared the MicroScan WalkAway system, a conventional biochemical identification system (Dade MicroScan, Inc., Sacramento, Calif.), with the Vitek system (bioMerieux Vitek, Hazelwood, Mo. [analysis software version AMS-RO8.2]) for the identification of gram-negative bacteria. Three-hundred thirty-one nonurine isolates and 493 urine isolates were tested. For nonurinary isolates, there was 91.5% agreement between the two methods. For urinary isolates, there was 97.4% agreement between the two methods. Overall, there was 95% agreement between the two systems. The results suggest that the current version of the MicroScan WalkAway system with conventional panels is essentially comparable to the current Vitek system.

Automated identification systems are commonly used in clinical microbiology laboratories; two commonly used systems are the Vitek and MicroScan systems. Both systems are semiautomated systems with different formats that essentially incubate test panels, perform automated readings, and either can report results to a personal computer system or can be interfaced with a laboratory information system. Numerous evaluations of various versions of the systems described above have been published over the years, and recent evaluations have focused on the MicroScan rapid panels (2). Side-by-side evaluations of these two systems with conventional MicroScan identification panels have not been published in many years (3). In addition to hardware changes, many software changes and updates have occurred since earlier evaluations, and thus, it is difficult to judge the performance of the updated systems on the basis of earlier studies. In order to assess the current MicroScan conventional gram-negative panel system on the WalkAway-96 instrument, we conducted a prospective, side-by-side study comparing the WalkAway system, which has conventional gram-negative identification panels, with the Vitek system.

(This work was presented in part at the General Meeting of the American Society for Microbiology, Washington, D.C., 1995 [1a].)

Between September 1994 and November 1994, all isolates of gram-negative bacilli from a variety of body sites which were subject to automated identification (i.e., not spot tested) in the Clinical Microbiology Laboratory at the Hospital of the University of Pennsylvania were tested in parallel with both the Vitek system (bioMerieux Vitek, Hazelwood, Mo.) with analysis software version AMS-RO8.2 and the MicroScan WalkAway system with software version 20.20 (Dade MicroScan, Inc., Sacramento, Calif.). The gram-negative identification (GNI) card was used with the Vitek system, and conventional biochemical identification panels (urine combo 6 for urinary isolates and negative combo 16 for isolates from other body sites) were utilized with the WalkAway-96 system. All isolates were tested in parallel on the two systems, usually on the same day. Eighteen- to 24-hour-old isolates were used to set up all identification cards or panels.

WalkAway-96 instrument is an automated system which incubates microtiter identification and antimicrobial susceptibility testing panels, interprets biochemical results through the use of a photometric or fluorogenic reader, and generates computerized reports that can be interfaced with hospital mainframe information systems. Conventional panels utilize the photometric reader and provide identification results for gram-negative bacilli within 15 to 42 h, with reagents added automatically by the WalkAway instrument. Panels can be removed from the WalkAway instrument and read manually if verification is necessary. Panels for identification of gram-negative bacilli contain 29 modified conventional biochemicals and six antibiotics. The database associated with the MicroScan WalkAway instrument contains information for the identification of 59 groups, genera, or species of members of the family *Enterobacteriaceae* and 57 groups, genera, or species of nonfermentative and oxidase-positive gram-negative bacilli.

The Vitek system, originally developed for the National Aeronautics and Space Administration space program, is an automated photometric system used for identification and susceptibility testing of both gram-negative and gram-positive organisms. Currently, the GNI card contains 25 conventional biochemicals, three proprietary substrates, and one antibiotic. Identification cards can only be read on the automated reader-incubator. The database associated with the GNI card includes information on 47 species of members of the family *Enterobacteriaceae* and 41 species of other gram-negative organisms. Final identification is usually available after 4 to 18 h of incubation.

Vitek GNI cards were processed according to the manufacturer's specifications. MicroScan panels were inoculated with the MicroScan prompt inoculation system D, and panels were inoculated within 4 h. Purity plates were used for each isolate. Quality control for the Vitek GNI cards was performed with the start of each new lot, as was quality control for MicroScan biochemicals in conventional panels. Identifications were accepted from either system if the likelihood of that identification was greater than or equal to 85%.

* Corresponding author. Mailing address: Department of Pathology and Laboratory Medicine, University of Pennsylvania, 3400 Spruce St., Philadelphia, PA 19104-4283. Phone: (215) 662-6651. Fax: (215) 662-6655. Electronic mail address: Irv_Nachamkin@path1a.med.upenn.edu.

TABLE 1. Comparison of the MicroScan WalkAway system with the Vitek system for the identification of urinary and nonurinary isolates

Identification	No. of isolates	Microscan		Vitek	
		% Correct	Misidentification	% Correct	Misidentification
Acinetobacter baumanii	80	97.5	No identification ($n = 2$)	100	
Alcaligenes xylosoxidans	1	100		100	
Citrobacter amalonaticus	2	50	*Escherichia coli*	100	
Citrobacter diversus	13	100		100	
Citrobacter freundii	13	92.3	*Enterobacter agglomerans*	92.3	*Escherichia coli*
Enterobacter aerogenes	21	95.2	*Serratia fonticola*	100	
Enterobacter cloacae	43	90.7	*Enterobacter* sp. *Citrobacter freundii* *Yersinia enterocolitica* No identification	86.1	*Pseudomonas aeruginosa* *Citrobacter freundii* *Escherichia coli* *Klebsiella oxytoca* No identification ($n = 2$)
Enterobacter sakazakii	1	0	*Enterobacter cloacae*	100	
Enterobacter taylorae	1	100		100	
Escherichia coli	383	97.9	*Citrobacter amalonaticus* ($n = 2$) *Enterobacter aerogenes* *Escherichia fergusonii* No identification ($n = 3$)	99.5	*Pseudomonas aeruginosa* No identification
Klebsiella oxytoca	8	87.5	*Klebsiella ozaenae*	87.5	*Escherichia coli*
Klebsiella ozaenae	1	100		100	
Klebsiella pneumoniae	132	86.4	*Kluyvera ascorbata* No identification *Enterobacter aerogenes* ($n = 2$) *Escherichia coli*	99.2	No identification
Morganella morganii	10	100		100	
Proteus mirabilis	41	100		100	
Providencia rettgeri	5	100		100	
Providencia stuartii	3	66.6	*Pasteurella multocida*	100	
Proteus vulgaris	1	100		100	
Pseudomonas aeruginosa	39	82.1	*Vibrio fluvialis* *Alcoligenes xylosoxidans* *Pseudomonas fluorescens* ($n = 2$) No identification ($n = 3$)	84.6	*Enterobacter cloacae* *Stenotrophomonas* (*Xanthomonas*) *maltophilia* *Pseudomonas fluorescens* No identification ($n = 3$)
Burkholderia cepacia	2	100		100	
Pseudomonas fluorescens	2	100		1	No identification
Salmonella sp.	2	100		100	
Serratia marcescens	20	100		100	

Discordant results between the two systems were arbitrated with the API-20E identification system (bioMerieux Vitek). Statistical analysis was performed with InStat v2.0 (GraphPad Software, Inc., San Diego, Calif.).

During the 3-month parallel evaluation, 503 urinary isolates were tested with both the Vitek GNI and MicroScan urine combo panels. The results are summarized in Table 1. Sample labeling discrepancies occurred with 10 samples, and thus the results with 493 samples were included in the analysis of data. The MicroScan and Vitek systems showed 97.4% agreement (480 of 493). Sixteen genera and species were tested, with *Escherichia coli*, *Klebsiella pneumoniae*, and *Proteus mirabilis* accounting for 63.1, 16, and 6.9% of the isolates tested, respectively. The MicroScan system incorrectly identified six isolates at the genus level and one at the species level. Seven isolates were identified as "slow growers" after 18 h of incubation and required additional incubation time for identification. All seven isolates were correctly identified as *Acinetobacter baumanii* ($n = 6$) and *Alcaligenes xylosoxidans* ($n = 1$). The MicroScan system did not give an identification to four isolates. One isolate was misidentified by the Vitek system at the genus level, and one isolate was not identified. Overall, there were significantly more incorrect discordant results with the MicroScan system than with the Vitek system (11 versus 2, $P = 0.0265$, McNemar's paired test); however, for any particular organism, there was no difference between the methods.

From body sites other than urine, there were 331 identifications performed by the two systems. The MicroScan and Vitek systems showed 91.5% (303 of 331) agreement. Twenty-one genera and species were tested. *A. baumanii*, *Enterobacter cloacae*, *E. coli*, *K. pneumoniae*, and *Pseudomonas aeruginosa* accounted for 21.8, 9.7, 19.9, 16, and 11.8% of the isolates tested, respectively. The MicroScan system misidentified nine isolates at the genus level and five at the species level and did not identify six isolates. Eighty-two of the 331 isolates required greater than 18 h of incubation (24.8%) with the MicroScan system only. Sixty-one (74.4%) were *A. baumanii*, 9 were *P. aeruginosa*, 4 were *Stenotrophomonas* (*Xanthomonas*) *maltophilia*, and 3 were *Alcaligenes* spp. Four isolates were not identified with the additional incubation period. The Vitek system misidentified eight isolates at the genus level and one isolate at the species level and did not identify seven isolates. There were eight instances in which both systems incorrectly identified isolates at either the genus level or species level or in which both systems were unable to identify an isolate. Overall, there was no significant difference between the number of incorrect discordant results by the MicroScan system and that by the Vitek system (12 versus 8, $P = 0.5023$, McNemar's paired test).

Few recent studies evaluating the comparability of the current MicroScan conventional identification panels with other systems have been performed. Almost all recent studies have reported on the rapid identification panels (2). Early studies showed good performance of the conventional panels for identification of members of the family *Enterobacteriaceae* (1). Tenover et al. (3), however, found that the system had major difficulties in identifying non-glucose-fermenting gram-negative rods. Most commonly misidentified were isolates of *Pseudomonas putida*, *Pseudomonas fluorescens*, *S.* (*Xanthomonas*) *maltophilia*, and *A. xylosoxidans* subsp. *xylosoxidans*. More recently, Van Pelt et al. (4) evaluated an updated database version for gram-negative identification (V20) with clinical and stock isolates. The new database correctly identified 96.8 and 89.6% of clinical fermenters and nonfermenters, respectively, and showed high levels of probability with additional tests, identifying 99 and 96.6% of clinical fermenters and nonfermenters, respectively. With stock strains, the system correctly identified approximately 96% of the isolates tested.

We compared the newest version of MicroScan software (V20.20) with the WalkAway instrument in a side-by-side prospective comparison with the Vitek system (AMS-RO8.2) for the identification of gram-negative bacilli. Overall, there was 95% agreement between the MicroScan and Vitek systems. For nonurinary isolates, including nonfermenters, there was 91.5% agreement between the two systems. After resolution of discordant results, both systems had an error rate of 5 to 6%, which was not statistically significant. Good results were obtained for both fermenters and nonfermenters. However, a significant number of isolates, particularly *A. baumanii*, were not identified within 1 day of incubation and required additional incubation on the MicroScan system for identification. There was a good level of agreement between the MicroScan and Vitek systems in terms of identifying urinary tract isolates (97.4%). Of the discordant results between the two systems, the MicroScan system had a higher number of incorrect results than the Vitek system (11 versus 2). No specific problems were noted, however; for any particular organism, there was no significant difference between the two systems.

The MicroScan WalkAway system using the conventional dried gram-negative identification panels gave results essentially equivalent to those of the Vitek system. Although some statistically significant differences in the identification of urinary isolates were noted, we do not feel that overall these had important clinical implications.

This study was supported in part by Dade MicroScan, Inc.

The assistance of the staff of the Clinical Microbiology Laboratory at the University of Pennsylvania Medical Center is greatly appreciated.

REFERENCES

1. **Gavini, F., M. O. Husson, D. Izard, A. Bernigaud, and B. Quiviger.** 1988. Evaluation of Autoscan-4 for identification of members of the family *Enterobacteriaceae*. J. Clin. Microbiol. **26:**1586–1588.

1a. **Rhoads, S., L. Marinelli, C. A. Imperatrice, and I. Nachamkin.** 1995. Comparison of MicroScan WalkAway™ system and Vitek system for the identification of gram-negative bacteria, abstr. C-305, p. 53. *In* Abstracts of the 95th General Meeting of the American Society for Microbiology 1995. American Society for Microbiology, Washington, D.C.

2. **Stager, C. E., and J. R. Davis.** 1992. Automated systems for identification of microorganisms. Clin. Microbiol. Rev. **5:**302–327.

3. **Tenover, F. C., T. S. Mizuki, and L. G. Carlson.** 1990. Evaluation of autoSCAN-W/A Automated Microbiology system for the identification of nonglucose-fermenting gram-negative bacilli. J. Clin. Microbiol. **7:**1628–1634.

4. **Van Pelt, L., T. Felland, K. Link, S. Connell, A. Chipman, K. Fujii, D. Nothaft, J. O'Connor, A. Shum, and B. L. Zimmer.** 1994. Performance of the MicroScan V.20 Dried Gram Negative Panel Identification System database, abstr. C-248, p. 534. *In* Abstracts of the 94th General Meeting of the American Society for Microbiology 1994. American Society for Microbiology, Washington, D.C.